

Figure 1

The initial three residues MVD have been introduced due to restriction sites

P26A	0.38	1.02	-0.07	0.39	0.55	0.85	-0.06	0.4	0.85
MVD	FLGRAYGL	- PYLFWLAAI	- HRCQAIRKK	- RRIYDIEL	- VQPPQLTLQV	- GLCTLVAML	- RLRAEAQVK	- IEDPPFNSL	- YLLEMLWRL
0.18	0.43	0.83	0.2	0.45	0.83	0.32	0.47	0.83	
GQGGSP	TAM	- AVLLHEESM	- IALYLQQNWWTL	- RAKFKQLL	- SSCSSCPLSKI	- TYGPVFMCL	- QAKWRLQTL	- RPPIFRRL	- VSFIEFVGW
0.34	0.52	0.82	0.35	0.53	0.71	0.36			
YPLHEQHGM	- VEITPYKPTW	- CLGGLTMV	- EENLLDFVRF	- TYSAGINQI	- LLDFVRFMGV	- EGGVGWRHW	- HHHHHH	(SEQ ID NO:94)	
P26B	0.38	1.02	-0.07	0.39	0.85	-0.06	0.4	0.53	0.71
MVD	FLGRAYGL	- PYLFWLAAI	- HRCQAIRKK	- RRIYDIEL	- GLCTLVAML	- RLRAEAQVK	- IEDPPFNSL	- TYSAGINQI	- LLDFVRFMGV
0.36	0.83	0.2	0.45	0.83	0.32	0.47	0.83	0.34	
EGGVGWRHW	- IALYLQQNWWTL	- RAKFKQLL	- SSCSSCPLSKI	- TYGPVFMCL	- QAKWRLQTL	- RPPIFRRL	- VSFIEFVGW	- YPLHEQHGM	
0.52	0.82	0.35	0.85	0.18	0.43	0.55			
VEITPYKPTW	- CLGGLTMV	- EENLLDFVRF	- YLLEMLWRL	- GQGGSP	TAM	- AVLLHEESM	- VQPPQLTLQV	- HHHHHH	(SEQ ID NO:95)

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Hydrophobicity Index (Fauschere & Pliska)

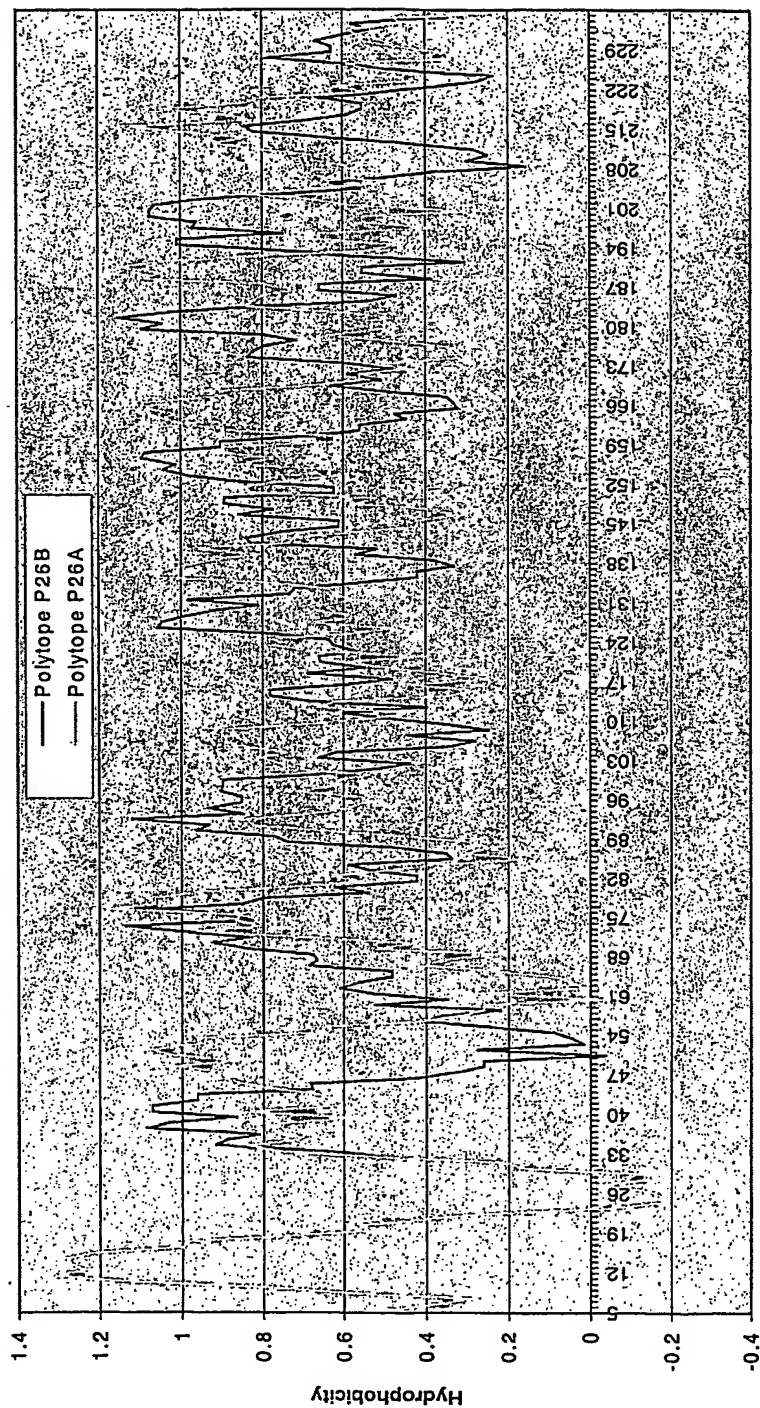


Figure 2

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Figure 3A gp350/PT26A

MEDPGFFNVEIPEFPFYPTCNVCTADVNTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENAT
 T-help epitope 70
 NLFLELLGAGELALTMRSKKLPIINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPY
 140
 IKWDNCNSTNITAVVRAOGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPDGNKFN
 T-help epitope 210
 ITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNNSILYVFYSGNGPKASGGDYCI
 280
 QSNIVFSDEIPASQDMPTNTTDDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLT
 350
 SGTPSGCENISGAFASNRTFDITVSGLGTA PKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGF
 420
 ADPNTTTGVDFLRGRAYGLPYLFWLA⁴²⁸AIHRCQAIRKKRRIYDLIELVQPPQ^{B8}LT^{A23}LQVGLCTLVAMLR^{B27}RLRAE^{B27}
^{B46}
 AOVKIEDPPFNSLYLLEMLWRLGQGSPTAMAVLLHEESMIALYLOQNW^{A2}WTLRAKFKQLLSSC^{A3}SSCPLSK
^{B60} ^{A2} ^{B62} ^{B35} ^{B57/A2} ^{B8} ^{A11}
 ITYGPVFMCLQAKWRLQTLRPPIFIRRLVSFIEFVGWYPLHEQHGMVEITPYKPTWCLGGLLT^{A24}MTVEENLL^{B8}
 DFVRFTYSAGIVQILLDFVRFMGVEGGVGWRHWHHHHHH^{B7}
 B44 ^{A24} ^{A2} ^{B44 (SEQ ID NO:96)}

Figure 3B gp350/PT26B

MEDPGFFNVEIPEFPFYPTCNVCTADVNTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENAT
 T-help epitope 70
 NLFLELLGAGELALTMRSKKLPIINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLIPETVPY
 140
 IKWDNCNSTNITAVVRAOGLDVTLP LSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPDGNKFN
 T-help epitope 210
 ITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNNSILYVFYSGNGPKASGGDYCI
 280
 QSNIVFSDEIPASQDMPTNTTDDITYVGDNATYSVPMVTSEDANSPNVTVTAFWAWPNNTETDFKCKWTLT
 350
 SGTPSGCENISGAFASNRTFDITVSGLGTA PKTLIITRTATNATTTTHKVIFSKAPESTTTSPTLNTTGF
 420
 ADPNTTTGVDFLRGRAYGLPYLFWLA⁴²⁸AIHRCQAIRKKRRIYDLIELGLCTLVAMLR^{B8}RLRAEAQ VKIEDPPF^{A23}
^{B27} ^{B27} ^{A2} ^{A3} ^{B60}
 NSLTYSAGIVQILLDFVRFMGVEGGVGWRHWIALYLOQNW^{A24}WTLRAKFKQLLSSC^{A2}SSCPLSKITYGPV^{B44}FM^{B57/A2}
^{B8} ^{B7} ^{B58} ^{B35} ^{B44} ^{A2} ^{B44}
 LQAKWRLQTLRPPIFIRRLVSFIEFVGWYPLHEQHGMVEITPYKPTWCLGGLLTMTVEENLLDFVRFYLL
 MLWRLGQGSPTAMAVLLHEESMVQPPQ^{A2}LT^{B62}LQVHHHHHH (SEQ ID NO:97)
^{B35} ^{B46}

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Figure 4A

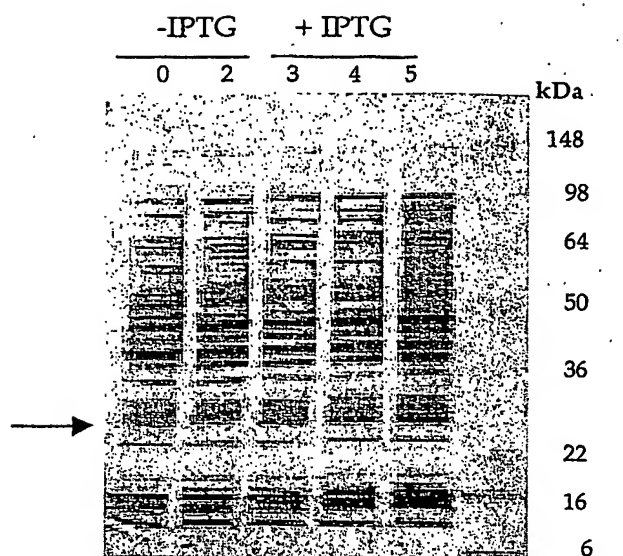


Figure 4B

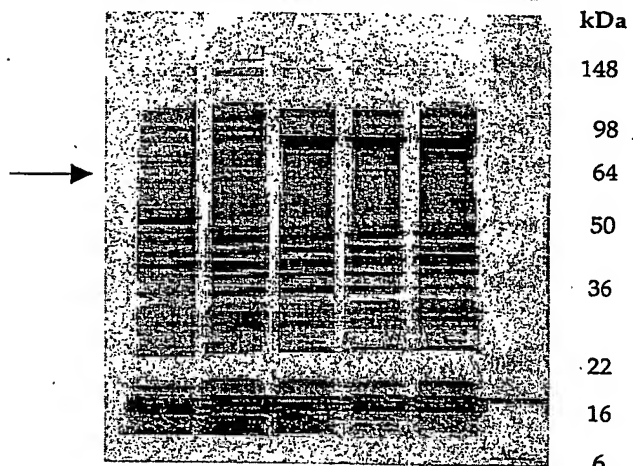


Figure 4C

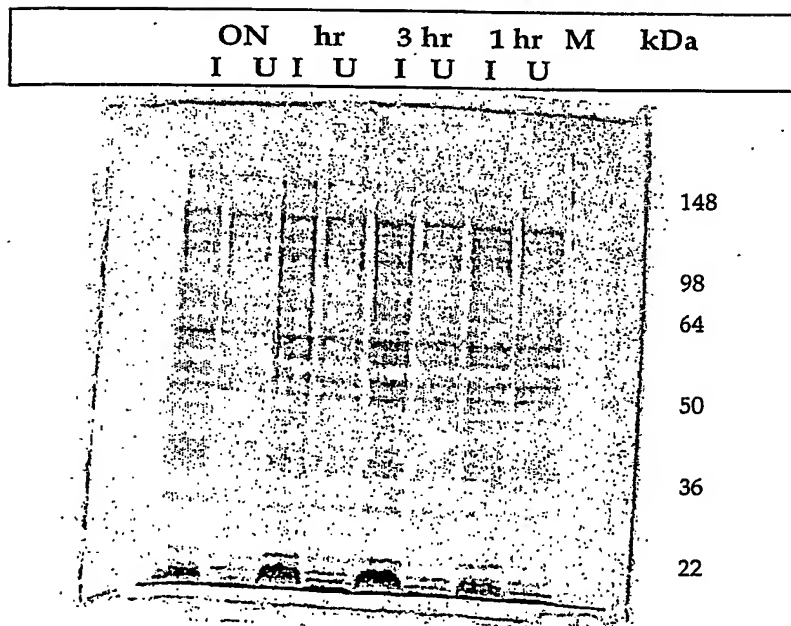


Figure 5

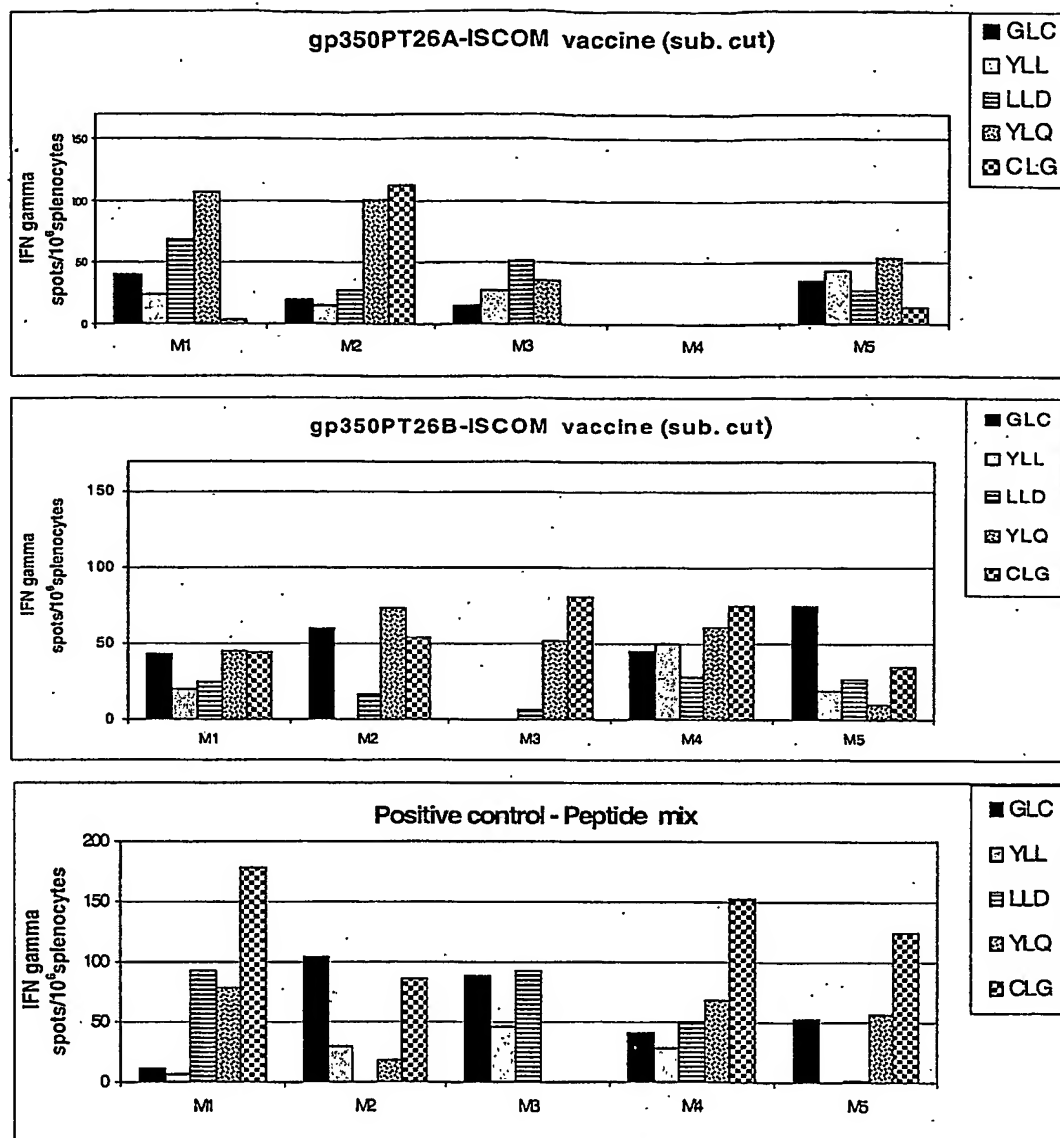


Figure 6

EBV-NPc_a
1.02 -0.07 0.82 0.98 -0.06 0.4 0.88 0.01 0.45 0.85
SSCSCPLSKI - HRCQAIRKK - CLGGLTMTV - LTAGFLIFL - RLRAEAQVK - IEDPPFNSL - LLSAWILTA - RRRWRRLTV - PYLFWLAAI - YLLEMLWRL -
0.18 0.64 0.85 0.20 0.67 0.83 0.32 0.71 0.34 0.78
GQGGSP TAM - VMSNTLLSAW - ALLVLYSFA - RAKFKQLL - IALYLOQNW - TYGPFVMCL - QAKWRLOTL - YLQONWWTL - YPLHEQHGM - CPLSKILL -
0.04
HHHHHH (SEQ ID NO:98)

HIVa															
0.98	-0.26	0.44	0.8	-0.16	0.44	0.76	-0.02	0.45	0.71						
IPVAVIALV - RLRPGGKK - ILKEPVHGV - PLVKLWYQL - RPKGKKKYKL - KYKLKHIVW - TWETWWTEYW - EIKDTKEAL - KRWILGLNK - KLWVTVVYGV -															
0.14	0.47	0.69	0.22	0.48	0.69	0.27	0.5	0.67	0.35	0.53					
KIEELRQHL - MTNNPPVP - VTLWQRPLV - WASRELERF - LLWKGEHAV - YTAFTPSI - IYQEPFKNLK - SLYNTVATL - AIRILQQL - AIFQSSMTK - VIYQYMDDL -															
0.61	0.36	0.57	0.59	0.57	0.04										
LVGPTPVNI - TPQDLNTML - YLAWVPAHK - ALVEICTEM - TLNAWVKV - HHHHHH (SEQ ID NO:99)															
HI values (n=3): 1.16 0.98 1.08 1.04 1.18 1.19 1.14 1.30 1.32 1.30 1.38 1.39 1.44 1.46 1.52 1.55 1.49 1.50 1.54 1.52 1.73 1.20															
HIVb															
0.44	0.45	0.57	0.14	0.69	0.22	0.8	0.61	0.98	0.5	0.47					
ILKEPVHGV - KRWILGLNK - TLNAWVKV - KIEELRQHL - YTAFTPSI - WASRELERF - PLVKLWYQL - LVGPTPVNI - IPVAVIALV - SLYNTVATL - MTNNPPVP -															
0.48	0.76	0.35	-0.26	0.59	0.71	0.57	0.67	-0.02	0.69						
LLWKGEHAV - TWETWWTEYW - AIFQSSMTK - RLRPGGKK - ALVEICTEM - KLWVTVVYGV - YLAWVPAHK - AIRILQQL - EIKDTKEAL - VTLWQRPLV -															
0.27	0.53	0.36	-0.16	0.44	0.04										
IYQEPFKNLK - VIYQYMDDL - TPQDLNTML - RPKGKKKYKL - KYKLKHIVW - HHHHHH (SEQ ID NO:100)															
HI values (n=3): 1.46 1.16 1.40 1.05 1.71 1.63 2.39 2.09 1.95 1.45 1.71 1.59 0.85 0.68 1.04 1.87 1.95 1.22 1.34 0.94 1.49 1/16 0.73 0.64 0.32															

	0.94	-0.3	0.61	0.9	-0.07	0.47	0.82	0.15	0.51	0.75
LLFNILGWV - KTSERSQR - FULLADRV - LLFLLADA - RLGVRATRK - GVAGALVAFK - LPGCSFSIF - RMYVGGVEHR - VAGALVAFK - DLMGYPLV -										
LIFCHSKKK - ILACYGAGV - HMWNFISGI - QLFTFSPRR - VGIYLLPNR - FWAKHMMWF - YLVTRHADV - LSAFSLHSY - WMNRLIAFA - YLLPRRGRL -	0.33	0.55	0.73	0.34	0.56	0.72	0.34	0.56	0.68	0.35
YLWAYQATV - RLIVFPDLGV - TLFGGAYMSK - IPFYGKAI - VLVGGLVLA - CTCGSSDLY - HHHHHH (SEQ ID NO:101)	0.58	0.67	0.41	0.61	0.67	0.44	0.04			

[illegible]

HI values (n=3): 1.46 1.68 1.55 1.44 1.61 1.67 2.24 2.07 1.93 0.73 0.10 0.38 1.35 2.36 2.19 1.87 1.65 1.41 1.88 1.77 1.58 1.17 1.23 1.59 1.22

Figure 9

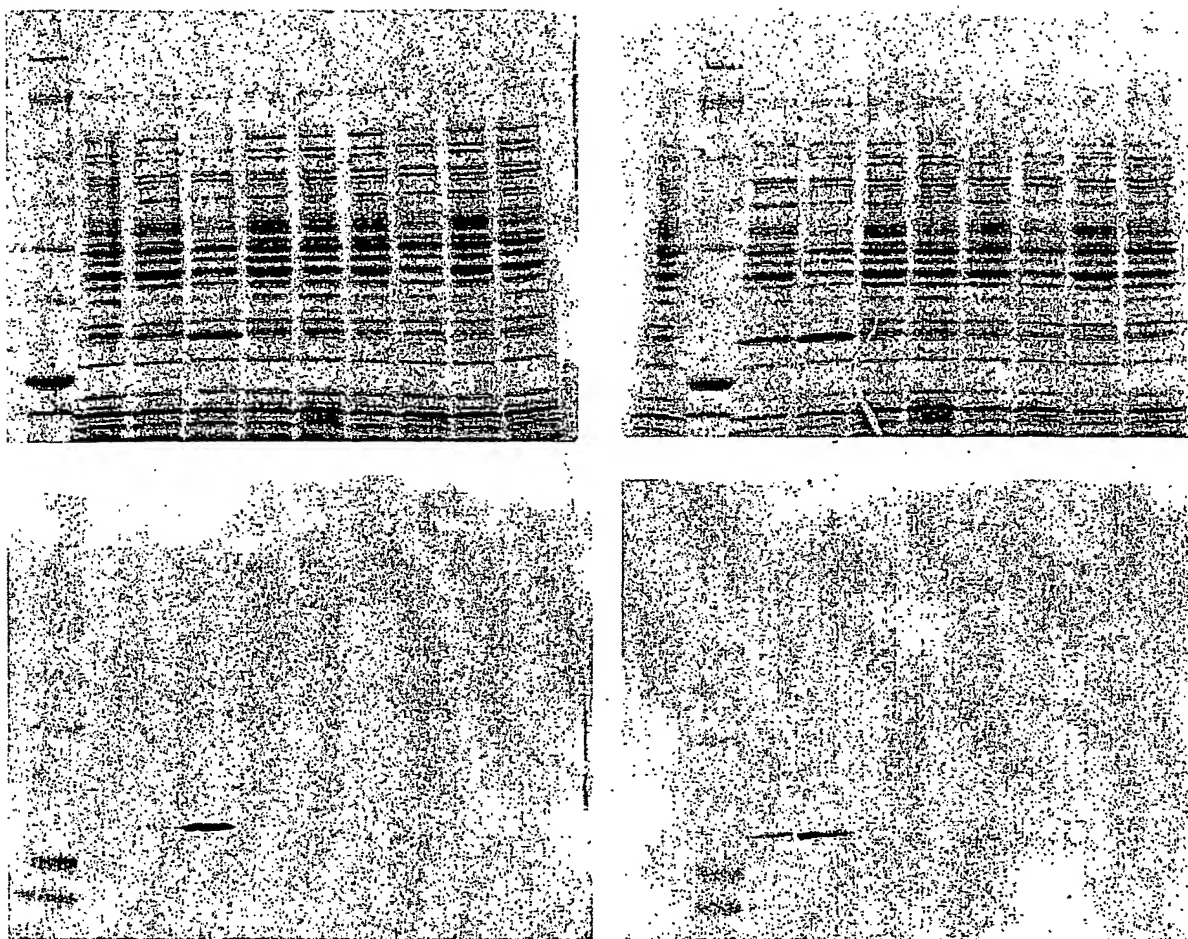
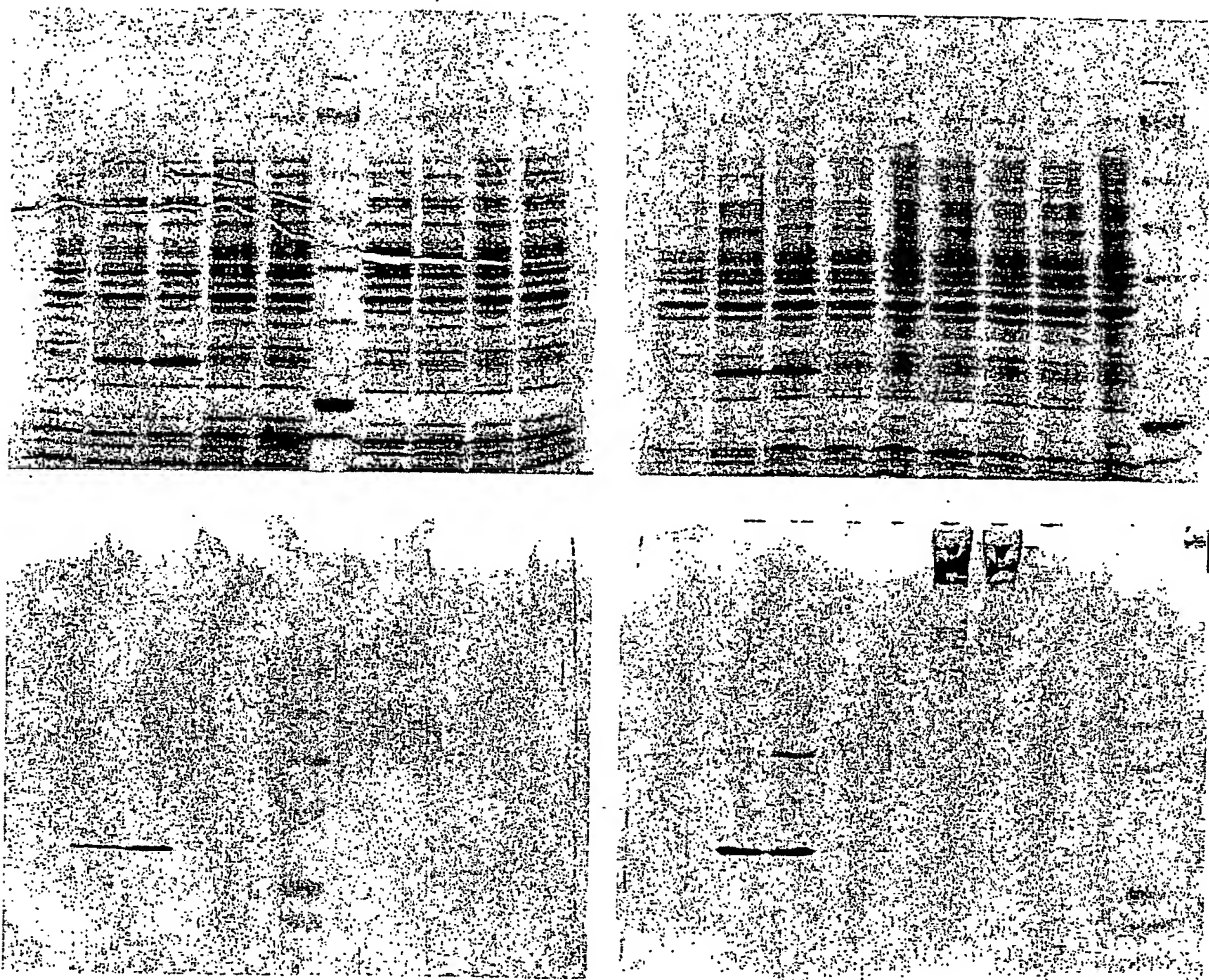


Figure 10



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